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1. **Global identifiability of nonlinear models of biological systems**
Audoly, S.; Bellu, G.; D'Angio, L.; Saccomani, M.P.; Cobelli, C.;
Biomedical Engineering, IEEE Transactions on
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AbstractPlus | References | Full Text: PDF(192 KB) IEEE JNL

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Industrial Electronics, Control and Instrumentation, 1991. Proceedings. IECON '91., 19
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28 Oct.-1 Nov. 1991 Page(s):2318 - 2322 vol.3
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2. **Error analysis of the Poisson P/sup 3/M force field scheme for particle-based sim biological systems**
Marreiro, D.; Aboud, S.; Saraniti, M.; Eisenberg, R.;
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3. **Improving analog simulation speed using selective matrix update**
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1. **Model identification of signal transduction networks from data using a state regu**
Gadkar, K.G.; Varner, J.; Doyle, F.J., III;
Systems Biology, IEE
Volume 2, Issue 1, 14 March 2005 Page(s):17 - 30
AbstractPlus | Full Text: PDF(631 KB) IEE JNL

2. **Cluster analysis for gene expression data: a survey**
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Volume 16, Issue 11, Nov. 2004 Page(s):1370 - 1386
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4. **Deterministic small-world graphs and the eigenvalue power law of Internet**
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M.; Brenner, M.; Schreiter, M.; Gabl, R.; Plehnert, K.; Steinhauser, M.; Eckstein, G.; Sc
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1 Research papers: graph and tree-structured data: Substructure similarity search in graph databases

Xifeng Yan, Philip S. Yu, Jiawei Han

June 2005 **Proceedings of the 2005 ACM SIGMOD international conference on Management of data**

Full text available: pdf(385.59 KB) Additional Information: full citation, abstract, references

Advanced database systems face a great challenge raised by the emergence of massive, complex structural data in bioinformatics, chem-informatics, and many other applications. The most fundamental support needed in these applications is the efficient search of complex structured data. Since exact matching is often too restrictive, *similarity search of complex structures* becomes a vital operation that must be supported efficiently.In this paper, we investigate the issues of *substructure* ...

2 Modeling the brain with NCS and brainlab

Rich Drewes

June 2005 **Linux Journal**, Volume 2005 Issue 134

Full text available: html(20.01 KB) Additional Information: full citation, abstract

Maybe the "neural networks" of Computer Science aren't so "neural" after all. This project takes the simulation one step closer to the brain.

3 Link-based similarity: Partitioning of Web graphs by community topology

Hidehiko Ino, Mineichi Kudo, Atsuyoshi Nakamura

May 2005 **Proceedings of the 14th international conference on World Wide Web**

Full text available: pdf(193.04 KB) Additional Information: full citation, abstract, references, index terms

We introduce a stricter Web community definition to overcome boundary ambiguity of a Web community defined by Flake, Lawrence and Giles [2], and consider the problem of finding communities that satisfy our definition. We discuss how to find such communities and hardness of this problem.We also propose Web page partitioning by equivalence relation defined using the class of communities of our definition. Though the problem of efficiently finding all communities of our definition is NP-complete, w ...

Keywords: Web community, graph partitioning, maximum flow algorithm

4 Networks, control, and life-forms

Alexander Galloway, Eugene Thacker
February 2005 **ACM SIGGROUP Bulletin**, Volume 25 Issue 2

Full text available: pdf(177.85 KB) Additional Information: full citation, abstract, index terms

In this paper we explore the technological, philosophical and political aspects of networks through a series of condensed, interrelated analyses.

Keywords: computers and society, cyberculture, internet, multitude, netwars, networks, politics

5 Long papers: visualization and presentation: The centrality of pivotal points in the evolution of scientific networks

Chaomei Chen
January 2005 **Proceedings of the 10th international conference on Intelligent user interfaces**

Full text available: pdf(732.87 KB) Additional Information: full citation, abstract, references, index terms

In this paper, we describe the development of CiteSpace as an integrated environment for identifying and tracking thematic trends in scientific literature. The goal is to simplify the process of finding not only highly cited clusters of scientific articles, but also pivotal points and trails that are likely to characterize fundamental transitions of a knowledge domain as a whole. The trails of an advancing research field are captured through a sequence of snapshots of its intellectual structure ...

Keywords: betweenness centrality, information visualization, intellectual turning points, knowledge domain visualization, research fronts

6 Routing protocols and overlays: The peer sampling service: experimental evaluation of unstructured gossip-based implementations

Márk Jelasity, Rachid Guerraoui, Anne-Marie Kermarrec, Maarten van Steen
October 2004 **Proceedings of the 5th ACM/IFIP/USENIX international conference on Middleware**

Full text available: pdf(390.72 KB) Additional Information: full citation, abstract, references

In recent years, the gossip-based communication model in large-scale distributed systems has become a general paradigm with important applications which include information dissemination, aggregation, overlay topology management and synchronization. At the heart of all of these protocols lies a fundamental distributed abstraction: the <I>peer sampling</I> service. In short, the aim of this service is to provide every node with peers to exchange information with. Analytical studies re ...

7 Research track papers: Fast discovery of connection subgraphs

Christos Faloutsos, Kevin S. McCurley, Andrew Tomkins
August 2004 **Proceedings of the 2004 ACM SIGKDD international conference on Knowledge discovery and data mining**

Full text available: pdf(233.09 KB) Additional Information: full citation, abstract, references, index terms

We define a *connection subgraph* as a small subgraph of a large graph that best captures the relationship between two nodes. The primary motivation for this work is to provide a paradigm for exploration and knowledge discovery in large social networks graphs. We present a formal definition of this problem, and an ideal solution based on electricity analogues. We then show how to accelerate the computations, to produce approximate, but high-quality connection subgraphs in real time on very ...

8

Research track posters: Mining scale-free networks using geodesic clustering
Andrew Y. Wu, Michael Garland, Jiawei Han
August 2004 **Proceedings of the 2004 ACM SIGKDD international conference on Knowledge discovery and data mining**
Full text available: pdf(606.55 KB) Additional Information: full citation, abstract, references, index terms

Many real-world graphs have been shown to be scale-free---vertex degrees follow power law distributions, vertices tend to cluster, and the average length of all shortest paths is small. We present a new model for understanding scale-free networks based on multilevel geodesic approximation, using a new data structure called a *multilevel mesh*.Using this multilevel framework, we propose a new kind of graph clustering for data reduction of very large graph systems such as social, biological, ...

Keywords: clustering, graphs, scale-free networks, social networks

9 Cell Modeling Using Agent-Based Formalisms
Kenneth Webb, Tony White
July 2004 **Proceedings of the Third International Joint Conference on Autonomous Agents and Multiagent Systems - Volume 3**
Full text available: pdf(365.80 KB) Additional Information: full citation, abstract, index terms

The systems biology community is building increasingly complex models and simulations of cells and other biological entities. This community is beginning to look at alternatives to traditional representations such as those provided by ordinary differential equations (ODE). Making use of the object-oriented (OO) paradigm, the Unified Modeling Language (UML) and Real-time Object-Oriented Modeling (ROOM) visual formalisms, we describe a simple model that includes membranes with lipid bilayers, mult ...

10 Special Section on Science of Network Design: Methodological frameworks for large-scale network analysis and design
Antonis Papachristodoulou, Lun Li, John C. Doyle
July 2004 **ACM SIGCOMM Computer Communication Review**, Volume 34 Issue 3
Full text available: pdf(847.60 KB) Additional Information: full citation, abstract, references

This paper emphasizes the need for methodological frameworks for analysis and design of large scale networks which are independent of specific design innovations and their advocacy, with the aim of making networking a more systematic engineering discipline. Networking problems have largely confounded existing theory, and innovation based on intuition has dominated design. This paper will illustrate potential pitfalls of this practice. The general aim is to illustrate universal aspects of theo ...

11 Knowledge and education: Visualizing multiple network perspectives
Misja N. Hoebe, Rien Bosma
June 2004 **Proceedings of the conference on Dutch directions in HCI**
Full text available: pdf(103.99 KB) Additional Information: full citation, abstract, references

In this paper, we describe a tool for displaying multiple network perspectives, where each perspective is a relation in which resources on the network are linked to others via a shared property. Every change or addition of perspective can be seen as a context switch, providing the actor with various navigation paths through a complex, multidimensional information space. This tool will attempt to capture and visualize the increasing amount of information coming available through the tools and sta ...

Keywords: constructivism, semantic web, social networks, visualization

12 Features: The Hitchhiker's Guide to Biomorphic Software
Kenneth N Lodding
June 2004 **Queue**, Volume 2 Issue 4
Full text available: pdf(1.26 MB) html(37.31 KB) Additional Information: full citation, index terms

13 Optimistic Methods: Time warp - connection oriented
Nasser Kalantery
May 2004 **Proceedings of the eighteenth workshop on Parallel and distributed simulation**
Full text available: pdf(110.14 KB) Additional Information: full citation, abstract, references

Conservative parallel discrete event simulation takes a connection-oriented approach to inter-process communication. Conservative processes modeling physical entities are connected via channels that represent physical links in the target system. By contrast, optimistic strategy and its implementation in Time Warp machine, take a connectionless approach where a process can communicate freely with any other process without prior connection. This paper presents the case for a connection-oriented op ...

14 Bioinformatics (BIO): Combining analysis and synthesis in a model of a biological cell
Ken Webb, Tony White
March 2004 **Proceedings of the 2004 ACM symposium on Applied computing**
Full text available: pdf(537.11 KB) Additional Information: full citation, abstract, references

We have previously described a top-down analytical approach, Cell Assembly Kit (CellAK), based on the object-oriented (OO) paradigm and the Unified Modeling Language (UML) and Real-Time Object-Oriented Methodology (ROOM) formalisms, for developing models and simulations of cells and other biological entities. In this approach, models consist of a hierarchy of containers (ex: cytosol), active objects with behavior (ex: enzymes, lipid bilayers, transport proteins), and passive small molecules (ex: ...

Keywords: analysis, autopoiesis, cell simulation, reactive systems, synthesis

15 Representing experimental biological data in metabolic networks
Tim Dwyer, Hardy Rolletschek, Falk Schreiber
January 2004 **Proceedings of the second conference on Asia-Pacific bioinformatics - Volume 29**
Full text available: pdf(752.02 KB) Additional Information: full citation, abstract, references

This paper describes a novel approach to representing experimental biological data in metabolic networks. The aim is to allow biologists to visualise and analyse the data in the context of the underlying processes. Biological networks can be modelled as graphs and visualised using graph drawing methods. We present a general method for mapping experimental data onto nodes and edges of a graph and to visualise the data-enriched networks in 2 1/2 dimensions such that the data is easy to understand. ...

Keywords: graph drawing, metabolic networks, metabolic profiling, time series data, visualisation

16 Evolving genetic regulatory networks using an artificial genome
Jennifer Hallinan, Janet Wiles
January 2004 **Proceedings of the second conference on Asia-Pacific bioinformatics -**

Volume 29

Full text available: pdf(138.30 KB) Additional Information: full citation, abstract, references

Boolean models of genetic regulatory networks (GRNs) have been shown to exhibit many of the characteristic dynamics of real GRNs, with gene expression patterns settling to point attractors or limit cycles, or displaying chaotic behaviour, depending upon the connectivity of the network and the relative proportions of excitatory and inhibitory interactions. This range of behaviours is only apparent, however, when the nodes of the GRN are updated synchronously, a biologically implausible state of a ...

Keywords: asynchrony, fuzzy limit cycles, genetic regulatory networks

17 Articles on microarray data mining: Mining biologically active patterns in metabolic pathways using microarray expression profiles

Hiroshi Mamitsuka, Yasushi Okuno, Atsuko Yamaguchi

December 2003 **ACM SIGKDD Explorations Newsletter**, Volume 5 Issue 2

Full text available: pdf(221.59 KB) Additional Information: full citation, abstract, references

We present a new probabilistic framework for analyzing a metabolic pathway with microarray expression profiles. Our purpose is to find biologically significant paths and patterns in a given metabolic pathway. Our approach first builds a Markov model using a graph structure of a known metabolic pathway, and then estimates parameters of a mixture of the Markov models using microarray data, based on an EM algorithm. In our experiments, we used a main pathway of glycolysis to evaluate the effectiven ...

Keywords: Markov Models, finite mixture models, metabolic pathways, microarray profiles, model-based clustering

18 Knowledge management session 1: visual: Visualization of Communication Patterns in Collaborative Innovation Networks - Analysis of Some W3C Working Groups

Peter A. Gloor, Rob Laubacher, Scott B. C. Dynes, Yan Zhao

November 2003 **Proceedings of the twelfth international conference on Information and knowledge management**

Full text available: pdf(309.40 KB) Additional Information: full citation, abstract, references, index terms

Collaborative Innovation Networks (COINs) are groups of self-motivated individuals from various parts of an organization or from multiple organizations, empowered by the Internet, who work together on a new idea, driven by a common vision. In this paper we report first results of a project that examines innovation networks by analyzing the e-mail archives of some W3C (WWW consortium) working groups. These groups exhibit ideal characteristics for our purpose, as they form truly global networks wo ...

Keywords: collaborative applications, collaborative innovation network, knowledge management, social network analysis, temporal information visualization

19 Research track: Algorithms for estimating relative importance in networks

Scott White, Padhraic Smyth

August 2003 **Proceedings of the ninth ACM SIGKDD international conference on Knowledge discovery and data mining**

Full text available: pdf(412.86 KB) Additional Information: full citation, abstract, references, citings, index terms

Large and complex graphs representing relationships among sets of entities are an increasingly common focus of interest in data analysis---examples include social networks,

Web graphs, telecommunication networks, and biological networks. In interactive analysis of such data a natural query is "which entities are most important in the network relative to a particular individual or set of individuals?" We investigate the problem of answering such queries in this paper, focusing in particular on de ...

Keywords: Markov chains, PageRank, graphs, relative importance, social networks

20 A computer algebra approach to biological systems 

Reinhard Laubenbacher

August 2003 **Proceedings of the 2003 international symposium on Symbolic and algebraic computation**

Full text available: pdf(63.77 KB) Additional Information: full citation, abstract, references

This paper focuses on dynamic networks over finite fields and applications to the modeling and analysis of biological networks using tools from computer algebra, in particular gene regulatory networks, and agent-based simulations of processes in computational immunology.

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21 Simulation: A multi-agent system for the quantitative simulation of biological networks
Salim Khan, Ravi Makkena, Foster McGeary, Keith Decker, William Gillis, Carl Schmidt
July 2003 **Proceedings of the second international joint conference on Autonomous agents and multiagent systems**
Full text available: pdf(154.41 KB) Additional Information: full citation, abstract, references, citings, index terms

We apply the multi-agent system (MAS) platform to the task of biological network simulation. In this paper, we describe the simulation of signal transduction (ST) networks using the DECAF [9] MAS architecture. Unlike previous approaches that relied on systems of differential equations (DE), the distributed framework of MAS scales well and allows us to model large, highly interconnected ST pathways. This scalability is achieved by adopting a hybrid strategy that factors macro-level measures, such ...

Keywords: multi-agent systems, simulation

22 Source-adaptive multilayered multicast algorithms for real-time video distribution
Brett J. Vickers, Célio Albuquerque, Tatsuya Suda
December 2000 **IEEE/ACM Transactions on Networking (TON)**, Volume 8 Issue 6
Full text available: pdf(206.61 KB) Additional Information: full citation, references, citings

Keywords: congestion control, feedback control, multilayered video

23 Algorithms for identifying Boolean networks and related biological networks based on matrix multiplication and fingerprint function
Tatsuya Akutsu, Satoru Miyano, Satoru Kuhara
April 2000 **Proceedings of the fourth annual international conference on Computational molecular biology**
Full text available: pdf(608.05 KB) Additional Information: full citation, abstract, references

Due to the recent progress of the DNA microarray technology, a large number of gene expression profile data are being produced. How to analyze gene expression data is an important topic in computational molecular biology Several studies have been done using the Boolean network as a model of a genetic network This paper proposes efficient algorithms for identifying Boolean networks of bounded indegree and related biological

networks, where identification of a Boolean network can be formalized ...

24 Biological Neural Networks in Invertebrate Neuroethology and Robotics. Editors: Randall D. Beer, Roy E. Ritzmann, Thomas McKenna (Academic Press, Inc., Harcourt Brace Jovanovich, 1993)

Glenn Becker

October 1996 **ACM SIGART Bulletin**, Volume 7 Issue 4

Full text available: pdf(129.22 KB) Additional Information: full citation, abstract

This book is the result of a workshop held in the fall of 1991 at the National Academy of Sciences Study Center in Woods Hole, MA. The workshop was entitled "Locomotion Control of Legged Invertebrates" and it was sponsored by the Office of Naval Research. The purpose of the workshop was to bring together researchers studying neural control of sensory and motor systems in invertebrates and researchers building legged robots. This type of cross-discipline work is often beneficial for both groups. ...

25 Pattern recognition with a pulsed neural network

Judith Dayhoff

May 1991 **Proceedings of the conference on Analysis of neural network applications**

Full text available: pdf(1.16 MB) Additional Information: full citation, references, index terms

26 Load balancing loosely synchronous problems with a neural network

G. C. Fox, W. Furmanski

January 1988 **Proceedings of the third conference on Hypercube concurrent computers and applications: Architecture, software, computer systems, and general issues - Volume 1**

Full text available: pdf(2.90 MB) Additional Information: full citation, abstract, references, citings, index terms

Hopfield and Tank have introduced the use of neural networks for the solution of optimization problems such as the traveling salesman problem. Here we show how to generalize this method to decompose loosely synchronous problems onto parallel machines and in particular the hypercube. In this case, decomposition or load balancing can be formulated graph theoretically in terms of optimal partitioning of the computational graph into N = 2

27 Hypercube algorithms for neural network simulation: the *Crystal_Accumulator* and the *Crystal Router*

G. C. Fox, W. Furmanski

January 1988 **Proceedings of the third conference on Hypercube concurrent computers and applications: Architecture, software, computer systems, and general issues - Volume 1**

Full text available: pdf(466.00 KB) Additional Information: full citation, abstract, references, citings, index terms

We discuss communication algorithms relevant for neural network modeling on distributed memory concurrent computers with a hypercube topology. Full, intermediate (medium range) and sparse network connectivities are analyzed. We point out that the flexible hypercube topology allows for the efficient implementation of the broad class of network algorithms with variety of connectivity patterns. We find algorithms index, crystal_router, fold an ...

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